

Qy	421	Thr***AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeu	440
Db	1261	ACAGGGGCTGAAGGGGAAGCAAGGCCTCTTGATCTTAGGGGACAACATTTTCAACTTCTC	1320
Qy	441	ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala	460
Db	1321	CCATTTGGGTCTGGGAGGAGAATGTGCCCTGGAGTCAATCTGGCTACTTCGGGAATGGCA	1380
Qy	461	ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGln	480
Db	1381	ACACTTCTTGCATCTCTTATTCACTGCTTTGACTTGCAAGTGCTGGGTCCACAAGGACAG	1440
Qy	481	IleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValPro	500
Db	1441	ATATTGAAGGGTGGTGACGCCAAAGTTAGCATGGAAGAGAGCCGGCCTCACTGTTCCA	1500
Qy	501	ArgAlaHisSerLeuValCysValProLeuAlaArgIleGlyValAlaSerLysLeuLeu	520
Db	1501	AGGGCACATAGTCTTGTCTGTGTTCCACTTGCAAGGATCGGCGTTGCATCTAAACTCCTT	1560
Qy	521	Ser 521	
Db	1561	TCT 1563	

RESULT 9

```

AF135484
LOCUS      AF135484                  1722 bp    mRNA    linear    PLN 02-AUG-1999
DEFINITION Glycine max cytochrome P450 monooxygenase CYP93C1v2p (CYP93C1v2)
            mRNA, complete cds.
ACCESSION  AF135484
VERSION    AF135484.1  GI:5059123
KEYWORDS    .
SOURCE      Glycine max.
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 1722)
  AUTHORS   Steele,C.L., Gijzen,M., Qutob,D. and Dixon,R.A.
  TITLE     Molecular characterization of the enzyme catalyzing the aryl
            migration reaction of isoflavonoid biosynthesis in soybean
  JOURNAL   Arch. Biochem. Biophys. 367 (1), 146-150 (1999)
  MEDLINE   99306846
  PUBMED    10375412
REFERENCE   2  (bases 1 to 1722)
  AUTHORS   Steele,C.L., Gijzen,M., Qutob,D. and Dixon,R.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-MAR-1999) Plant Biology, Noble Foundation, 2510 Sam
            Noble Pkwy, Ardmore, OK 73402, USA
FEATURES             Location/Qualifiers
     source            1. .1722
                       /organism="Glycine max"
                       /db_xref="taxon:3847"
     gene              1. .1722
                       /gene="CYP93C1v2"
     CDS               36. .1601

```

```

/gene="CYP93C1v2"
/function="2-hydroxyisoflavanone synthase"
/note="The functional expression of this cDNA demonstrated
2-hydroxyisoflavanone synthase activity"
/codon_start=1
/product="cytochrome P450 monooxygenase CYP93C1v2p"
/protein_id="AAD38929.1"
/db_xref="GI:5059124"
/translation="MLLELALGLLVLALFLHLRPTPTAKSKALRHLPNPPSPKPRLPF
IGHLHLLKDKLLHYALIDLSKKHGPLESLYFGSMPTVVASTPELFLQTHEATSFN
TRFQTSAIRRLTYDSSVAMVPFGPYWKEVRKLIIMNDLLNATTVNKLRPLRTOQIRKFL 160
RVMAQCAEAQKPLDTEELLKWTNSTISMMMLGEAEIIRDIAREVLKIFGEYSITDFI
WPLKHLKVGKYEKRIDDILNKFDPVVERVIKKRREIVRRRKNGEVVEGEVSGVFLDTL
LEFAEDETMEIKITKDHKGLVVDFFSAGTDSATAVEWALAEINNPVKLEKAREEV
YSVVGKDRLVDEYDTQNLPIRAIVKETFRMHPLPVKKRCKTEECINGYVIPEGAL
ILFNWQVGRDPKYWDRPSEFRPERFLETGAEGEAGPLDLRGQHFQQLLPFGSGRRMCP
GVNLATSGMATLLASLIQCFDLQVLGPQGQILKGGDAKVSMEERAGLTVPRAHSLVCV
PLARIGVASKLLS"

```

misc_difference 445

```

/gene="CYP93C1v2"
/note="difference compared to GenBank Accession Number
AF022462; causes change of P to L (aa 140)"
/replace="c"

```

misc_difference 502

```

/gene="CYP93C1v2"
/note="difference compared to GenBank Accession Number
AF022462; causes change of T to I (aa 156)"
/replace="c"

```

misc_difference 918

```

/gene="CYP93C1v2"
/note="difference compared to GenBank Accession Number
AF022462; causes change of E to K (aa 295)"
/replace="g"

```

misc_difference 1612..1620

```

/gene="CYP93C1v2"
/note="9 bp insertion compared to GenBank Accession Number
AF022462"
/replace=""

```

BASE COUNT 470 a 422 c 407 g 423 t
ORIGIN

Alignment Scores:

Pred. No.:	1.52e-259	Length:	1722
Score:	2267.00	Matches:	454
Percent Similarity:	87.14%	Conservative:	0
Best Local Similarity:	87.14%	Mismatches:	67
Query Match:	94.62%	Indels:	0
DB:	8	Gaps:	0

US-09-857-581-66 (1-521) x AF135484 (1-1722)

```

Qy      1 MetLeuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgPro 20
      |||
Db      36 ATGTTGCTTGAACCTTGCACTTGGTTTATTGGTTTTGGCTCTGTTTCTGCACTTGCGTCCC 95
      |||
Qy      21 ThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro***Pro 40
      |||

```

Db 96 ACACCCACTGCAAAATCAAAAGCACTTCGCCATCTCCCAAACCCACCAAGCCCAAGGCT 155
 Qy 41 ArgLeuProPheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla*** 60
 Db 156 CGTCTTCCCTTCATAGGACACCTTCATCTCTTAAAGACAAACTTCTCCACTACGCACTC 215
 Qy 61 IleAspLeuSerLysLysHisGlyProLeuPheSer*****PheGlySerMetProThr 80
 Db 216 ATCGACCTCTCCAAAAACATGGTCCCTTATTCTCTCTACTTTGGCTCCATGCCAACC 275
 Qy 81 ValValAlaSerThrProGluLeuPheLysLeuPheLeuGln*****GluAlaThrSer 100
 Db 276 GTTGTTCCTCCACACCAGAAATTGTTCAAGCTCTTCTCCAAACGCACGAGGCAACTTCC 335
 Qy 101 Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp*****ValAla 120
 Db 336 TTCAACACAAGGTTCCAAACCTCAGCCATAAGACGCCTCACCTATGATAGCTCAGTGGCC 395
 Qy 121 *****Pro***GlyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeuLeu 140
 Db 396 ATGTTTCCCTTCGGACCTTACTGGAAGTTCGTGAGGAAGCTCATCATGAACGACCTTCTC 455
 Qy 141 AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***Leu 160
 Db 456 AACGCCCACTGTAAACAAGTTGAGGCTTTGAGGACCAACAGATCCGCAAGTTCTCTT 515
 Qy 161 Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeu 180
 Db 516 AGGGTTATGGCCCAAGGCGCAGAGGCACAGAAGCCCTTGACTTGACCGAGGAGCTTCTG 575
 Qy 181 LysTrp***AsnSerThr***SerMetMet***LeuGlyGluAlaGluGluIleArgAsp 200
 Db 576 AAATGGACCAACAGCACCATCTCCATGATGATGCTCGGCGAGGCTGAGGAGATCAGAGAC 635
 Qy 201 IleAlaArgGluValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***Pro 220
 Db 636 ATCGCTCGCGAGGTTCTTAAGATCTTTGGCGAATACAGCCTCACTGACTTCATCTGGCCA 695
 Qy 221 LeuLys***LeuLysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPhe 240
 Db 696 TTGAAGCATCTCAAGGTTGAAAGTATGAGAAGAGGATCGACGACATCTTGAACAAGTTC 755
 Qy 241 AspProValValGluArgValIleLysLysArgArg***IleValArgArgArg***Asn 260
 Db 756 GACCCTGTCTGTTGAAAGGTCATCAAGAAGCGCCGTGAGATCGTGAGGAGGAGAAAGAAC 815
 Qy 261 GlyGlu*****GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAla 280
 Db 816 GGAGAGGTTGTTGAGGTTGAGGTCAGCGGGGTTTCTTGACACTTGCTTGAATTCGCT 875
 Qy 281 GluAspGluThr***GluIleLysIleThrLys***IleLysGlyLeuValValAsp 300
 Db 876 GAGGATGAGACCATGGAGATCAAAATCACAAGGACCACATCAAGGGTCTTGTGTCGAC 935
 Qy 301 ***PheSerAlaGly***AspSerThrAla***ThrGluTrpAlaLeuAlaGluLeu 320
 Db 936 TTTTCTCGGCAGGAACAGACTCCACAGCGGTGGCAACAGAGTGGGCATTGGCAGAACTC 995

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE 1 (bases 1 to 1824)
AUTHORS Siminszky, B., Corbin, F.T., Ward, E.R., Fleischmann, T.J. and Dewey, R.E.
TITLE Expression of a soybean cytochrome P450 monooxygenase cDNA in yeast and tobacco enhances the metabolism of phenylurea herbicides
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (4), 1750-1755 (1999)
MEDLINE 99145622
PUBMED 9990096
REFERENCE 2 (bases 1 to 1824)
AUTHORS Siminszky, B., Dewey, R.E. and Corbin, F.T.
TITLE Direct Submission
JOURNAL Submitted (04-SEP-1997) Crop Science, North Carolina State University, Box 7620, Raleigh, NC 27695, USA

FEATURES Location/Qualifiers
source 1..1824
/organism="Glycine max"
/db_xref="taxon:3847"
gene 1..1824
/gene="CYP93C1"
CDS 54..1619
/gene="CYP93C1"
/note="cytochrome P450 monooxygenase"
/codon_start=1
/product="CYP93C1p"
/protein_id="AAB94591.1"
/db_xref="GI:2739006"
/translation="MLLELALGLLVLALFLHLRPTPTAKSKALRHLNPPSPKPRLPF
IGHLHLLKDKLLHYALIDLKKGHGLPLFSLYFGSMPTVVASTPELFLQLTHEATSFN
TRFQTSAIRRLTYDSSVAMVPFGPYWKFFVRKLIMNDLPNATTVNKLRPLRTQQTRKFL
RVMAQGAEAQKPLDLTEELLKWTNSTISMMLGEAEEIRDIAREVLKIFGEYSLTDFI
WPLKHLKVGKYEKRIDDLNKFDPPVVERVIKKRREIVRRRKNGEVVEGEVSGVFLDTL
LEFAEDETMEIKITKDHIEGLVVDFFSAGTDSTAVATEWALAEILNNPKVLEKAREEV
YSVVGKDRLLVDEVDTONLPYIRAI VKETFRMHPPLPVVVKRKCTEECEINGYVIPEGAL
ILFNWQVGRDPKYWDRPSEFRPERFLETGAEGEAGPLDLRGQHFQLLPFGSGRRMCP
GVNLATSGMATLLASLIQCFDLQVLGPQGQILKGGDAKVSMEERAGLTVPRAHSLVCV
PLARIGVASKLLS"

BASE COUNT 497 a 448 c 416 g 463 t
ORIGIN

Alignment Scores:

Pred. No.:	1.3e-257	Length:	1824
Score:	2251.00	Matches:	451
Percent Similarity:	86.76%	Conservative:	1
Best Local Similarity:	86.56%	Mismatches:	69
Query Match:	93.95%	Indels:	0
DB:	8	Gaps:	0

US-09-857-581-66 (1-521) x AF022462 (1-1824)

Qy 1 MetLeuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgPro 20
|||||
Db 54 ATGTTGCTTGAACCTTGCACTTGTTTATTGGTTTGGCTCTGTTTCTGCACTTGCGTCCC 113
Qy 21 ThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro***Pro 40
||||| ||| ||||||||||||||||||||||||||||||||||||||| |||

Db 114 ACACCCACTGCAAAATCAAAAGCACTTCGCCATCTCCCAAACCCACCAAGCCCAAAGCCT 173
 Qy 41 ArgLeuProPheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla*** 60
 |||||
 Db 174 CGTCTTCCCTTCATAGGACACCTTCATCTCTTAAAAGACAAACTTCTCCACTACGCACTC 233
 Qy 61 IleAspLeuSerLysLysHisGlyProLeuPheSer*****PheGlySerMetProThr 80
 |||||
 Db 234 ATCGACCTCTCCAAAAACATGGTCCCCTTATTCTCTCTCTACTTTGGCTCCATGCCAACCC 293
 Qy 81 ValValAlaSerThrProGluLeuPheLysLeuPheLeuGln*****GluAlaThrSer 100
 |||||
 Db 294 GTTGTTGCCTCCACACCAGAATTGTTCAAGCTCTTCCTCCAAACGCACGAGGCAACTTCC 353
 Qy 101 Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp*****ValAla 120
 |||
 Db 354 TTCAACACAAGGTTCCAAACCTCAGCCATAAGACGCCTCACCTATGATAGCTCAGTGGCC 413
 Qy 121 *****Pro***GlyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeuLeu 140
 |||
 Db 414 ATGGTTCCCTTCGGACCTTACTGGAAGTTCGTGAGGAAGCTCATCATGAACGACCTTCCC 473
 Qy 141 AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***Leu 160
 |||||
 Db 474 AACGCCACCACTGTAAACAAGTTGAGGCCTTTGAGGACCCAACAGACCCGCAAGTTCCTT 533
 Qy 161 Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeu 180
 |||
 Db 534 AGGGTTATGGCCCAAGGCGCAGAGGCACAGAAGCCCCTTGACTTGACCGAGGAGCTTCTG 593
 Qy 181 LysTrp***AsnSerThr***SerMetMet***LeuGlyGluAlaGluGluIleArgAsp 200
 |||||
 Db 594 AAATGGACCAACAGCACCATCTCCATGATGATGCTCGGCGAGGCTGAGGAGATCAGAGAC 653
 Qy 201 IleAlaArgGluValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***Pro 220
 |||||
 Db 654 ATCGCTCGCGAGGTTCTTAAGATCTTTGGCGAATACAGCCTCACTGACTTCATCTGGCCA 713
 Qy 221 LeuLys***LeuLysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPhe 240
 |||||
 Db 714 TTGAAGCATCTCAAGGTTGGAAAGTATGAGAAGAGGATCGACGACATCTTGAACAAGTTC 773
 Qy 241 AspProValValGluArgValIleLysLysArgArg***IleValArgArgArg***Asn 260
 |||||
 Db 774 GACCTGTCTGTTGAAAGGGTCATCAAGAAGCGCCGTGAGATCGTGAGGAGGAGAAAGAAC 833
 Qy 261 GlyGlu*****GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAla 280
 |||||
 Db 834 GGAGAGGTTGTTGAGGGTGAGGTCAGCGGGGTTTTCCTTGACACTTTGCTTGAATTCGCT 893
 Qy 281 GluAspGluThr***GluIleLysIleThrLys*****IleLysGlyLeuValValAsp 300
 |||||
 Db 894 GAGGATGAGACCATGGAGATCAAAATCACCAAGGACCACATCGAGGGTCTTGTGTCGAC 953
 Qy 301 ***PheSerAlaGly***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeu 320
 |||||
 Db 954 TTTTCTCGGCAGGAACAGACTCCACAGCGGTGGCAACAGAGTGGGCATTGGCAGAACTC 1013

Qy	321	IleAsnAsnPro***ValLeu*****AlaArgGluGlu***TyrSerValValGlyLys	340
Db	1014	ATCAACAATCCTAAGGTGTTGGAAAAGGCTCGTGAGGAGGTCTACAGTGTGTGGGAAAG	1073
Qy	341	Asp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys	360
Db	1074	GACAGACTTGTGGACGAAGTTGACACTCAAACCTTCCTTACATTAGAGCAATCGTGAAG	1133
Qy	361	GluThrPheArgMetHisProProLeuProValValLysArgLysCys***GluGluCys	380
Db	1134	GAGACATTCCGCATGCACCCGCCACTCCCAGTGGTCAAAGAAAGTGCACAGAAGAGTGT	1193
Qy	381	***IleAsnGly***Val***ProGluGlyAlaLeu*****PheAsnValTrpGlnVal	400
Db	1194	GAGATTAATGGATATGTGATCCCAGAGGGAGCATTGATTCTCTTCAATGTATGGCAAGTA	1253
Qy	401	Gly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu	420
Db	1254	GGAAGAGACCCCAAATACTGGGACAGACCATCGGAGTTCCGTCCTGAGAGGTTCTAGAG	1313
Qy	421	Thr***AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeu	440
Db	1314	ACAGGGGCTGAAGGGGAAGCAGGGCCTCTTGATCTTAGGGGACAACATTTTCAACTTCTC	1373
Qy	441	ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala	460
Db	1374	CCATTTGGGTCTGGGAGGAGAATGTGCCCTGGAGTCAATCTGGCTACTTCGGGAATGGCA	1433
Qy	461	ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGln	480
Db	1434	ACACTTCTTGCATCTCTTATTTCAGTGCTTCGACTTGCAAGTGCTGGGTCCACAAGGACAG	1493
Qy	481	IleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValPro	500
Db	1494	ATATTGAAGGGTGGTGACGCCAAAGTTAGCATGGAAGAGAGCCGGCCTCACTGTTCCA	1553
Qy	501	ArgAlaHisSerLeuValCysValProLeuAlaArgIleGlyValAlaSerLysLeuLeu	520
Db	1554	AGGGCACATAGTCTTGTCTGTGTTCCACTTGCAAGGATCGGCGTTGCATCTAAACTCCTT	1613
Qy	521	Ser 521	
Db	1614	TCT 1616	

Glycine.

REFERENCE 1 (bases 1 to 1824)

AUTHORS Jung,W., Yu,O., Lau,S.M., O'Keefe,D.P., Odell,J., Fader,G. and McGonigle,B.

TITLE Identification and expression of isoflavone synthase, the key enzyme for biosynthesis of isoflavones in legumes

JOURNAL Nat. Biotechnol. 18 (2), 208-212 (2000)

MEDLINE 20124255

PUBMED 10657130

REFERENCE 2 (bases 1 to 1824)

AUTHORS Jung,W., Yu,O., Odell,J., Fader,G. and McGonigle,B.

TITLE Direct Submission

JOURNAL Submitted (18-OCT-1999) Nutrition and Health, DuPont, P.O. Box 80402, Wilmington, DE 19880-0402, USA

FEATURES Location/Qualifiers

source 1..1824

/organism="Glycine max"

/db_xref="taxon:3847"

gene 1..1824

/gene="ifs2"

CDS 54..1619

/gene="ifs2"

/codon_start=1

/product="isoflavone synthase 2"

/protein_id="AAF34520.1"

/db_xref="GI:6979522"

/translation="MLLELALGLLVLALFLHLRPTPTAKSKALRHLNPPSPKPRLPF IGHLHLLKDKLLHYALIDLSKKHGPLFSLYFGSMPTVVASTPELFLQTHEATSFN TRFQTSAIRRLTYDSSVAMVPFGPYWKFVRKLI MN DLPNATTVNKLRPLRTQQTRKFL RVMAQGAEAQPLDLTEELLKWTNSTISMMMLGEAAEIRDIAREVLKIFGEYSLTDFI WPLKHLKVGKYEKRIDDILNKFDPVVERVIKKRREIVRRRNKEVVEGEVSGVFLDTL LEFAEDETMEIKITKDHIEGLVVDFFSAGTDSTAVATEWALAE LINNPKVLEKAREEV YSVVGKDRLVDEVDTQNLPIRAIVKETFRMHPLPVVKRKCTEECEINGYVIPEGAL ILFNVWQVGRDPKYWDRPSEFRPERFLETGAEGEAGPLDLRGQHFQLLPFGSGRRMC P GVNLATSGMATLLASLIQCFLQVLGPQGQILKGGDAKVSMEERAGLTVPRAHSLVCV PLARIGVASKLLS"

BASE COUNT 497 a 448 c 416 g 463 t

ORIGIN

Alignment Scores:

Pred. No.:	1.3e-257	Length:	1824
Score:	2251.00	Matches:	451
Percent Similarity:	86.76%	Conservative:	1
Best Local Similarity:	86.56%	Mismatches:	69
Query Match:	93.95%	Indels:	0
DB:	8	Gaps:	0

US-09-857-581-66 (1-521) x AF195799 (1-1824)

Qy	1	MetLeuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgPro	20
Db	54	ATGTTGCTTGAACCTGCACTTGGTTTATTGGTTTTGGCTCTGTTTCTGCACTTGCGTCCC	113
Qy	21	ThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro***Pro	40
Db	114	ACACCCACTGCAAAATCAAAAGCACTTCGCCATCTCCCAAACCCACCAAGCCCAAGCCT	173

Qy	41	ArgLeuProPheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla***	60
Db	174	CGTCTTCCCTTCATAGGACACCTTCATCTCTTAAAGACAAACTTCTCCACTACGCACTC	233
Qy	61	IleAspLeuSerLysLysHisGlyProLeuPheSer*****PheGlySerMetProThr	80
Db	234	ATCGACCTCTCCAAAAACATGGTCCCTTATTCTCTCTCTACTTTGGCTCCATGCCAACC	293
Qy	81	ValValAlaSerThrProGluLeuPheLysLeuPheLeuGln*****GluAlaThrSer	100
Db	294	GTTGTTGCCTCCACACCAGAATTGTTCAAGCTCTTCCTCCAAACGCACGAGGCAACTTCC	353
Qy	101	Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp*****ValAla	120
Db	354	TTCAACACAAGGTTCCAAACCTCAGCCATAAGACGCCTCACCTATGATAGCTCAGTGGCC	413
Qy	121	*****Pro***GlyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeuLeu	140
Db	414	ATGGTTCCCTTCGGACCTTACTGGAAGTTCGTGAGGAAGCTCATCATGAACGACCTTCCC	473
Qy	141	AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***Leu	160
Db	474	AACGCCACCACTGTAAACAAGTTGAGGCCTTTGAGGACCCAACAGACCCGCAAGTTCCTT	533
Qy	161	Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeu	180
Db	534	AGGGTTATGGCCCAAGGCGCAGAGGCACAGAAGCCCCTTGACTTGACCGAGGAGCTTCTG	593
Qy	181	LysTrp***AsnSerThr***SerMetMet***LeuGlyGluAlaGluGluIleArgAsp	200
Db	594	AAATGGACCAACAGCACCATCTCCATGATGATGCTCGGCGAGGCTGAGGAGATCAGAGAC	653
Qy	201	IleAlaArgGluValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***Pro	220
Db	654	ATCGCTCGCGAGGTTCTTAAGATCTTTGGCGAATACAGCCTCACTGACTTCATCTGGCCA	713
Qy	221	LeuLys***LeuLysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPhe	240
Db	714	TTGAAGCATCTCAAGGTTGGAAGTATGAGAAGAGGATCGACGACATCTTGAACAAGTTC	773
Qy	241	AspProValValGluArgValIleLysLysArgArg***IleValArgArgArg***Asn	260
Db	774	GACCTGTCTGTTGAAAGGGTCATCAAGAAGCGCCGTGAGATCGTGAGGAGGAGAAAGAAC	833
Qy	261	GlyGlu*****GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAla	280
Db	834	GGAGAGGTTGTTGAGGGTGAGGTCAGCGGGGTTTTCCTTGACACTTTGCTTGAATTCGCT	893
Qy	281	GluAspGluThr***GluIleLysIleThrLys*****IleLysGlyLeuValValAsp	300
Db	894	GAGGATGAGACCATGGAGATCAAATCACCAAGGACCACATCGAGGCTTGTGTGTCGAC	953
Qy	301	***PheSerAlaGly***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeu	320
Db	954	TTTTTCTCGGCAGGAACAGACTCCACAGCGGTGGCAACAGAGTGGGCATTGGCAGAACTC	1013
Qy	321	IleAsnAsnPro***ValLeu*****AlaArgGluGlu***TyrSerValValGlyLys	340

```

Db 1014 ATCAACAATCCTAAGGTGTTGGAAAAGGCTCGTGAGGAGGTCTACAGTGTGTGGGAAAG 1073
Qy 341 Asp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys 360
Db 1074 GACAGACTTGTGGACGAAGTTGACACTCAAAACCTTCCTTACATTAGAGCAATCGTGAAG 1133
Qy 361 GluThrPheArgMetHisProProLeuProValValLysArgLysCys***GluGluCys 380
Db 1134 GAGACATTCCGCATGCACCCGCCACTCCCAGTGGTCAAAAAGAAAGTGCACAGAAGAGTGT 1193
Qy 381 ***IleAsnGly***Val***ProGluGlyAlaLeu*****PheAsnValTrpGlnVal 400
Db 1194 GAGATTAATGGATATGTGATCCAGAGGGAGCATTGATTCTCTTCAATGTATGGCAAGTA 1253
Qy 401 Gly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu 420
Db 1254 GGAAGAGACCCCAAATACTGGGACAGACCATCGGAGTTCCGTCCTGAGAGGTTCTTAGAG 1313
Qy 421 Thr***AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeu 440
Db 1314 ACAGGGGCTGAAGGGGAAGCAGGGCCTCTTGATCTTAGGGGACAACATTTTCAACTTCTC 1373
Qy 441 ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
Db 1374 CCATTTGGGTCTGGGAGGAGAATGTGCCCTGGAGTCAATCTGGCTACTTCGGAATGGCA 1433
Qy 461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGln 480
Db 1434 ACACTTCTTGCATCTCTTATTTCAGTGCTTCGACTTGCAAGTGCTGGGTCCACAAGGACAG 1493
Qy 481 IleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValPro 500
Db 1494 ATATTGAAGGGTGGTGACGCCAAAGTTAGCATGGAAGAGAGCCGGCCTCACTGTTCCA 1553
Qy 501 ArgAlaHisSerLeuValCysValProLeuAlaArgIleGlyValAlaSerLysLeuLeu 520
Db 1554 AGGGCACATAGTCTTGTCTGTGTTCCACTTGCAAGGATCGGCGTTGCATCTAAACTCCTT 1613
Qy 521 Ser 521
Db 1614 TCT 1616

```

RESULT 12

AF195819

LOCUS AF195819 1902 bp DNA linear PLN 23-MAR-2000

DEFINITION Glycine max isoflavone synthase 2 (ifs2) gene, complete cds.

ACCESSION AF195819

VERSION AF195819.1 GI:7288454

KEYWORDS

SOURCE Glycine max.

ORGANISM Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

REFERENCE 1 (bases 1 to 1902)

AUTHORS Jung,W., Yu,O., Lau,S.M., O'Keefe,D.P., Odell,J., Fader,G. and McGonigle,B.

TITLE Identification and expression of isoflavone synthase, the key enzyme for biosynthesis of isoflavones in legumes

JOURNAL Nat. Biotechnol. 18 (2), 208-212 (2000)

MEDLINE 20124255

PUBMED 10657130

REFERENCE 2 (bases 1 to 1902)

AUTHORS Jung,W., Yu,O., Odell,J., Fader,G. and McGonigle,B.

TITLE Direct Submission

JOURNAL Submitted (18-OCT-1999) Nutrition and Health, DuPont, PO Box 80402, Wilmington, DE 19880-0402, USA

FEATURES

source Location/Qualifiers

1. .1902

/organism="Glycine max"

/db_xref="taxon:3847"

gene 1. .1902

/gene="ifs2"

mRNA join(1. .948,1085. .1902)

/gene="ifs2"

/product="isoflavone synthase 2"

CDS join(52. .948,1085. .1753)

/gene="ifs2"

/note="cytochrome P450"

/codon_start=1

/product="isoflavone synthase 2"

/protein_id="AAF45143.1"

/db_xref="GI:7288455"

/translation="MLLELALGLLVLALFLHLRPTPTAKSKALRHLNPPSPKPRLPF IGHLHLLKDKLLHYALIDLKSKKHGPLFSLYFGSMPTVVASTPELFLQTHEATSFN TRFQTSAIRRLTYDSSVAMVPPGYPWKFVRKLI MN DLPNATTVNKLRPLRTQQTRKFL RVMAQGAEAQKPLDLTEELLKWTNSTISMMMLGEAEEIRDIAREVLKIFGEYSLTDFI WPLKHLKVGKYEKRIDDILNKFDPVVERVIKKRREIVRRRNKGEVVEGEVSGVFLDTL LEFAEDETMEIKITKDHIEGLVVDFFSAGTDSTAVATEWALAE LINNPKVLEKAREEV YSVVGKDRLVDEVDTQNLPIRAIVKETFRMHPLPVVKRKCTEECEINGYVIPEGAL ILFNWQVGRDPKYWDRPSEFRPERFLETGAEGEAGPLDLRGQHFQLLPFGSGRRMCP GVNLATSGMATLLASLIQCFDLQVLGPGQILKGGDAKVSMEERAGLTVPRAHSLVCV PLARIGVASKLLS"

BASE COUNT 517 a 455 c 440 g 490 t

ORIGIN

Alignment Scores:

Pred. No.:	1.06e-251	Length:	1902
Score:	2201.50	Matches:	451
Percent Similarity:	79.72%	Conservative:	1
Best Local Similarity:	79.54%	Mismatches:	69
Query Match:	91.88%	Indels:	46
DB:	8	Gaps:	1

US-09-857-581-66 (1-521) x AF195819 (1-1902)

```

Qy      1 MetLeuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgPro 20
      |||
Db      52 ATGTTGCTTGAACCTGCACTTGGTTTATTGGTTTGGCTCTGTTTCTGCACTTGGTCCC 111
      |||
Qy      21 ThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro***Pro 40
      |||

```

Db	112	ACACCCACTGCAAAATCAAAAGCACTTCGCCATCTCCCAAACCCACCAAGCCCAAGCCT	171
Qy	41	ArgLeuProPheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla***	60
Db	172	CGTCTTCCCTTCATAGGACACCTTCATCTCTTAAAAGACAACTTCTCCACTACGCACTC	231
Qy	61	IleAspLeuSerLysLysHisGlyProLeuPheSer*****PheGlySerMetProThr	80
Db	232	ATCGACCTCTCCAAAAACATGGTCCCTTATTCTCTCTCTACTTTGGCTCCATGCCAACC	291
Qy	81	ValValAlaSerThrProGluLeuPheLysLeuPheLeuGln*****GluAlaThrSer	100
Db	292	GTTGTTGCCTCCACACCAGAATTGTTCAAGCTCTTCTCCAAACGCACGAGGCAACTTC	351
Qy	101	Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp*****ValAla	120
Db	352	TTCAACACAAGGTTCCAAACCTCAGCCATAAGACGCCTCACCTATGATAGCTCAGTGGCC	411
Qy	121	*****Pro***GlyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeuLeu	140
Db	412	ATGGTTCCCTTCGGACCTTACTGGAAGTTCGTGAGGAAGCTCATCATGAACGACCTTCCC	471
Qy	141	AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***Leu	160
Db	472	AACGCCACCACTGTAAACAAGTTGAGGCCTTTGAGGACCCAACAGACCCGCAAGTTCCTT	531
Qy	161	Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeu	180
Db	532	AGGGTTATGGCCCAAGGCGCAGAGGCACAGAAGCCCCTTGACTTGACCGAGGAGCTTCTG	591
Qy	181	LysTrp***AsnSerThr***SerMetMet***LeuGlyGluAlaGluGluIleArgAsp	200
Db	592	AAATGGACCAACAGCACCATCTCCATGATGATGCTCGGCGAGGCTGAGGAGATCAGAGAC	651
Qy	201	IleAlaArgGluValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***Pro	220
Db	652	ATCGCTCGCGAGGTTCTTAAGATCTTTGGCGAATACAGCCTCACTGACTTCATCTGGCCA	711
Qy	221	LeuLys***LeuLysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPhe	240
Db	712	TTGAAGCATCTCAAGGTTGGAAGTATGAGAAGAGGATCGACGACATCTTGAACAAGTTC	771
Qy	241	AspProValValGluArgValIleLysLysArgArg***IleValArgArgArg***Asn	260
Db	772	GACCTGTCTGTTGAAAGGGTCATCAAGAAGCGCCGTGAGATCGTGAGGAGGAGAAAGAAC	831
Qy	261	GlyGlu*****GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAla	280
Db	832	GGAGAGGTTGTTGAGGGTGAGGTCAGCGGGGTTTTCCTTGACACTTGCTTGAATTCTGCT	891
Qy	281	GluAspGluThr***GluIleLysIleThrLys*****IleLysGlyLeuValVal---	299
Db	892	GAGGATGAGACCATGGAGATCAAAATCACCAAGGACCACATCGAGGGTCTTGTTGTCTGTG	951
Qy	299	-----	299
Db	952	AGTTTCCTGCTTCATTTCATTGATCGAAATATGCAGTATTTTGTTAACAAGAGATCGAGAA	1011

Qy 299 ----- 299

Db 1012 TTGACATTTATATATTCATGTGGTGGCAATTAATTAACGGTACGCATTCTTAATCGATAT 1071

Qy 300 -----Asp***PheSerAlaGly***AspSerThrAla*****ThrGluTr 315
 ||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1072 TGTGTATGTGCAGGACTTTTTCTCGGCAGGAACAGACTCCACAGCGGTGGCAACAGAGTG 1131

Qy 315 pAlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*****AlaArgGluGlu***Ty 335
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1132 GGCATTGGCAGAACTCATCAACAATCCTAAGGTGTTGGAAAAGGCTCGTGAGGAGGTCTA 1191

Qy 335 rSerValValGlyLysAsp***LeuValAspGluValAspThrGlnAsnLeuProTyrIl 355
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1192 CAGTGTGTGGGAAAGGACAGACTTGTGGACGAAGTTGACACTCAAACCTTCCTTACAT 1251

Qy 355 eArgAlaIleValLysGluThrPheArgMetHisProProLeuProValValLysArgLy 375
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1252 TAGAGCAATCGTGAAGGAGACATTCCGCATGCACCCGCCACTCCAGTGGTCAAAAAGAAA 1311

Qy 375 sCys***GluGluCys***IleAsnGly***Val***ProGluGlyAlaLeu*****Ph 395
 |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1312 GTGCACAGAAGAGTGTGAGATTAATGGATATGTGATCCAGAGGGAGCATTGATTCTCTT 1371

Qy 395 eAsnValTrpGlnValGly***Asp***LysTyrTrpAspArgProSerGlu***ArgPr 415
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1372 CAATGTATGGCAAGTAGGAAGAGACCCCAAATACTGGGACAGACCATCGGAGTTCCGTCC 1431

Qy 415 oGluArgPheLeuGluThr***AlaGluGlyGluAla*****LeuAspLeuArgGly** 435
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1432 TGAGAGGTTCTTAGAGACAGGGGCTGAAGGGGAAGCAGGGCCTCTTGATCTTAGGGGACA 1491

Qy 435 *HisPheGlnLeuLeuProPheGlySerGlyArg***MetCysProGlyVal***LeuAl 455
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1492 ACATTTTCAACTTCTCCCATTGTTGGGTCTGGGAGGAGAATGTGCCCTGGAGTCAATCTGGC 1551

Qy 455 aThrSerGly***AlaThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLe 475
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1552 TACTTCGGGAATGGCAACACTTCTTGATCTCTTATTCAGTGCTTCGACTTGCAAGTGCT 1611

Qy 475 uGlyProGlnGlyGlnIleLeuLysGly***AspAlaLysValSerMetGluGluArgAl 495
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1612 GGGTCCACAAGGACAGATATTGAAGGGTGGTGACGCCAAAGTTAGCATGGAAGAGAGAGC 1671

Qy 495 aGlyLeuThrValProArgAlaHisSerLeuValCysValProLeuAlaArgIleGlyVa 515
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1672 CGGCCTCACTGTTCCAAGGGCACATAGTCTTGTCTGTGTTCCACTTGCAAGGATCGGCGT 1731

Qy 515 lAlaSerLysLeuLeuSer 521
 ||||| ||||| ||||| |||||

Db 1732 TGCATCTAAACTCCTTTCT 1750

RESULT 13

AF195818

LOCUS AF195818 1800 bp DNA linear PLN 23-MAR-2000

DEFINITION Glycine max isoflavone synthase 1 (ifs1) gene, partial cds.

ACCESSION AF195818
 VERSION AF195818.1 GI:7288452
 KEYWORDS .
 SOURCE Glycine max.
 ORGANISM Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.
 REFERENCE 1 (bases 1 to 1800)
 AUTHORS Jung,W., Yu,O., Lau,S.M., O'Keefe,D.P., Odell,J., Fader,G. and
 McGonigle,B.
 TITLE Identification and expression of isoflavone synthase, the key
 enzyme for biosynthesis of isoflavones in legumes
 JOURNAL Nat. Biotechnol. 18 (2), 208-212 (2000)
 MEDLINE 20124255
 PUBMED 10657130
 REFERENCE 2 (bases 1 to 1800)
 AUTHORS Jung,W., Yu,O., Odell,J., Fader,G. and McGonigle,B.
 TITLE Direct Submission
 JOURNAL Submitted (18-OCT-1999) Nutrition and Health, DuPont, PO Box 80402,
 Wilmington, DE 19880-0402, USA
 FEATURES Location/Qualifiers
 source 1..1800
 /organism="Glycine max"
 /db_xref="taxon:3847"
 gene <1..>1800
 /gene="ifs1"
 mRNA join(<1..893,1112..>1800)
 /gene="ifs1"
 /product="isoflavone synthase 1"
 CDS join(<1..893,1112..1780)
 /gene="ifs1"
 /note="cytochrome P450"
 /codon_start=3
 /product="isoflavone synthase 1"
 /protein_id="AAF45142.1"
 /db_xref="GI:7288453"
 /translation="LELALGLFVLALFLHLRPTPSAKSKALRHLNPPSPKPRLPFIG
 HLHLLKDKLLHYALIDLKKGHLPLFSLSFGSMPTVVASTPELFLQTHEATSFNTR
 FQTSAIRRLTYDNSVAMVPFGPYWKFVRKLIMNDLLNATTVNKLRLRTQQIRKFLRV
 MAQSAAEQKPLDVTEELLKWTNSTISMMMLGEAAEIRDIAREVLKIFGEYSLTDFIWP
 LKYLKVGKYEKRIDDILNKFDPVVERVIKKRREIVRRRKNGEVVEGEASGVFLDTLLE
 FAEDETMEIKITKEQIKGLVVDFFSAGTDSTAVATEWALAEINNPRVLQKAREEVYS
 VVGKDRLVDEVDTQNLPIRAIVKETFRMHPPLPVVKRKCTEECEINGYVIPEGALVL
 FNVWQVGRDPKYWDRPSEFRPERFLETGAEGEAGPLDLRGQHFQLLPFGSGRRMCPGV
 NLATSGMATLLASLIQCFDLQVLGPQGQILKGDDAKVSMEEERAGLTVPRAHSLVCVPL
 ARIGVASKLLS".
 BASE COUNT 476 a 441 c 413 g 470 t
 ORIGIN

Alignment Scores:

Pred. No.:	3.04e-250	Length:	1800
Score:	2189.00	Matches:	451
Percent Similarity:	76.18%	Conservative:	0
Best Local Similarity:	76.18%	Mismatches:	68
Query Match:	91.36%	Indels:	74

Db	783	GTTGTTGAGGGCGAGGCCAGCGGCGTCTTCCTCGACACTTTGCTTGAATTCGCTGAGGAC	842
Qy	283	GluThr***GluIleLysIleThrLys*****IleLysGlyLeuValVal-----	299
Db	843	GAGACCATGGAGATCAAAATTACCAAGGAGCAAATCAAGGGCCTTGTTGT-CGTAAGTTT	901
Qy	299	-----	299
Db	902	CCTTCTTCTCTCCTACTTTATTACTTTCTTTCATTCATCATATGTATTGGCATTAAATAG	961
Qy	299	-----	299
Db	962	TATACTATATGAGAAAATATGTTACGCACTCACGGTGTAAGATATGTGGTGTTTTTTTA	1021
Qy	299	-----	299
Db	1022	AAAAGAGATACAGAAGTTGCTTTTATGCATGTATGTTAACGTATATTTACTCAAGTGGA	1081
Qy	300	-----Asp***PheSerAlaGly***AspSerThr	309
Db	1082	ACTAATTAATTCTCAATTTTGGGTATGTAGGACTTTTCTCTGCAGGGACAGATTCCACA	1141
Qy	310	Ala*****ThrGluTrpAlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*****	329
Db	1142	GCGGTGGCAACAGAGTGGGCATTGGCAGAGCTCATCAACAATCCCAGGGTGTTGCAAAAG	1201
Qy	330	AlaArgGluGlu***TyrSerValValGlyLysAsp***LeuValAspGluValAspThr	349
Db	1202	GCTCGTGAGGAGGTCTACAGTGTTGTGGGCAAAGATAGACTCGTTGACGAAGTTGACACT	1261
Qy	350	GlnAsnLeuProTyrIleArgAlaIleValLysGluThrPheArgMetHisProProLeu	369
Db	1262	CAAAACCTTCCTTACATTAGGGCCATTGTGAAGGAGACATTCCGAATGCACCCACCACTC	1321
Qy	370	ProValValLysArgLysCys***GluGluCys***IleAsnGly***Val***ProGlu	389
Db	1322	CCAGTGGTCAAAAGAAAGTGCACAGAAGAGTGTGAGATTAATGGGTATGTGATCCCAGAG	1381
Qy	390	GlyAlaLeu*****PheAsnValTrpGlnValGly***Asp***LysTyrTrpAspArg	409
Db	1382	GGAGCATTGTTCTTTTCAATGTTTGGCAAGTAGGAAGGGACCCCAAATACTGGGACAGA	1441
Qy	410	ProSerGlu***ArgProGluArgPheLeuGluThr***AlaGluGlyGluAla*****	429
Db	1442	CCATCAGAATTCCTGCCGAGAGGTTCTTAGAACTGGTGCTGAAGGGGAAGCAGGGCCT	1501
Qy	430	LeuAspLeuArgGly***HisPheGlnLeuLeuProPheGlySerGlyArg***MetCys	449
Db	1502	CTTGATCTTAGGGGCCAGCATTTCCAATCCTCCCATTGGGTCTGGGAGGAGAATGTGC	1561
Qy	450	ProGlyVal***LeuAlaThrSerGly***AlaThrLeuLeuAlaSerLeuIleGlnCys	469
Db	1562	CCTGGTGTCAATTGCGCTACTTCAGGAATGGCAACACTTCTGCATCTCTTATCCAATGC	1621
Qy	470	PheAspLeuGlnValLeuGlyProGlnGlyGlnIleLeuLysGly***AspAlaLysVal	489

Db 1622 TTTGACCTGCAAGTGCTGGGCCCTCAAGGACAAATATTGAAAGGTGATGATGCCAAAGTT 1681

Qy 490 SerMetGluGluArgAlaGlyLeuThrValProArgAlaHisSerLeuValCysValPro 509
 |||

Db 1682 AGCATGGAAGAGAGAGCTGGCCTCACAGTTCCAAGGGCACATAGTCTCGTTTGTGTTCCA 1741

Qy 510 LeuAlaArgIleGlyValAlaSerLysLeuLeuSer 521
 |||

Db 1742 CTTGCAAGGATCGGCGTTGCATCTAAACTCCTTTCT 1777

RESULT 14

AF195801

LOCUS AF195801 1501 bp mRNA linear PLN 16-FEB-2000

DEFINITION Medicago sativa isoflavone synthase 2 (ifs2) mRNA, partial cds.

ACCESSION AF195801

VERSION AF195801.1 GI:6979525

KEYWORDS

SOURCE Medicago sativa.

ORGANISM Medicago sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
 Medicago.

REFERENCE 1 (bases 1 to 1501)

AUTHORS Jung,W., Yu,O., Lau,S.M., O'Keefe,D.P., Odell,J., Fader,G. and McGonigle,B.

TITLE Identification and expression of isoflavone synthase, the key enzyme for biosynthesis of isoflavones in legumes

JOURNAL Nat. Biotechnol. 18 (2), 208-212 (2000)

MEDLINE 20124255

PUBMED 10657130

REFERENCE 2 (bases 1 to 1501)

AUTHORS Jung,W., Yu,O., Odell,J., Fader,G. and McGonigle,B.

TITLE Direct Submission

JOURNAL Submitted (18-OCT-1999) Nutrition and Health, DuPont, P.O. Box 80402, Wilmington, DE 19880-0402, USA

FEATURES Location/Qualifiers

source 1..1501

/organism="Medicago sativa"

/db_xref="taxon:3879"

gene <1..>1501

/gene="ifs2"

CDS <1..>1501

/gene="ifs2"

/codon_start=3

/product="isoflavone synthase 2"

/protein_id="AAF34522.1"

/db_xref="GI:6979526"

/translation="FLHLRPTPTAKSKALRHLPNPPSPKPRLPFIGHLHLLKDKLLHY
 ALIDLSKKHGPLFSLYFGSMPTVVASTPELFLQTHEATSFNTRFQTSAIRRLTYD
 SSVAMAPFGPYWKFVRKLIMNDLLNATTVNKLRLRTQQIRKFLRVMAQGAQAQKPLD
 LTEELLKWTNSTTSMMLGEABEIRDIAREVLKIFGEYSLTDFIRPLKHLKVGKYEKR
 IDDIILNKFDPVVERVIKKRREIVRRRKNGEVVEGEVSGVFLDTLLEFAEDETTEIKIT
 KDHKGLVVDFFSAGTDSTAVATEWALAEILNPNKVLEKAREEVSVVGKDRLVDEVD
 TQNLPIRAIVKETFRMHPPLPVVKRKCTEECEINGYVIPEGALILFNWQVGRDSKY
 WDRPSEFRPERFLETGAEGEARPLDLRGQHFQLLPFGSGRRMCPGVNLATSGMATLLA
 SLIQCFDLQVLGPQGQILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIG"